

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/302,195B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10    Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/302,195B

DATE: 07/30/2002

TIME: 14:11:21

Input Set : A:\26046400.ST25.txt

Output Set: N:\CRF3\07302002\I302195B.raw

**Does Not Comply**  
**Corrected Diskette Needed**

*pp 1-3*

3 <110> APPLICANT: Marchant, Roger E.  
 4 Qiu, Yongxing  
 5 Ruegsegger, Mark A.  
 7 <120> TITLE OF INVENTION: Surfactants That Mimic The Glycocalyx  
 9 <130> FILE REFERENCE: 26046/04000  
 11 <140> CURRENT APPLICATION NUMBER: 09/302,195B  
 12 <141> CURRENT FILING DATE: 1999-04-29  
 14 <160> NUMBER OF SEQ ID NOS: 10  
 16 <170> SOFTWARE: PatentIn version 3.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 3  
 20 <212> TYPE: PRT  
 C--> 21 <213> ORGANISM: Artificial/Unknown  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: PEPTIDE  
 25 <222> LOCATION: (1)..(3)  
 26 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
 29 <400> SEQUENCE: 1  
 31 Arg Gly Asp  
 32 1  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 4  
 37 <212> TYPE: PRT  
 C--> 38 <213> ORGANISM: Artificial/Unknown  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: PEPTIDE  
 42 <222> LOCATION: (1)..(4)  
 43 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
 46 <400> SEQUENCE: 2  
 48 Arg Gly Asp Ser  
 49 1  
 52 <210> SEQ ID NO: 3  
 53 <211> LENGTH: 5  
 54 <212> TYPE: PRT  
 C--> 55 <213> ORGANISM: Artificial/Unknown  
 57 <220> FEATURE:  
 58 <221> NAME/KEY: PEPTIDE  
 59 <222> LOCATION: (1)..(5)  
 60 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
 63 <400> SEQUENCE: 3  
 65 Arg Gly Asp Ser Pro  
 66 1 5  
 69 <210> SEQ ID NO: 4

*global  
 invalid response, per 1.823 d  
 Sequence Rules*

*(see item 10  
 on Error Summary  
 sheet)*

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70 <211> LENGTH: 4  
71 <212> TYPE: PRT  
C--> 72 <213> ORGANISM: Artificial/Unknown  
74 <220> FEATURE:  
75 <221> NAME/KEY: PEPTIDE  
76 <222> LOCATION: (1)..(4)  
77 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
80 <400> SEQUENCE: 4  
82 Arg Arg Ala Arg  
83 1  
86 <210> SEQ ID NO: 5  
87 <211> LENGTH: 6  
88 <212> TYPE: PRT  
C--> 89 <213> ORGANISM: Artificial/Unknown  
91 <220> FEATURE:  
92 <221> NAME/KEY: PEPTIDE  
93 <222> LOCATION: (1)..(6)  
94 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
97 <400> SEQUENCE: 5  
99 Arg Arg Arg Lys Arg Arg  
100 1 5  
103 <210> SEQ ID NO: 6  
104 <211> LENGTH: 7  
105 <212> TYPE: PRT  
C--> 106 <213> ORGANISM: Artificial/Unknown  
108 <220> FEATURE:  
109 <221> NAME/KEY: PEPTIDE  
110 <222> LOCATION: (1)..(8)  
111 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
114 <400> SEQUENCE: 6  
116 Pro Pro Arg Arg Ala Arg Val Thr  
117 1 5  
120 <210> SEQ ID NO: 7  
121 <211> LENGTH: 11  
122 <212> TYPE: PRT  
C--> 123 <213> ORGANISM: Artificial/Unknown  
125 <220> FEATURE:  
126 <221> NAME/KEY: PEPTIDE  
127 <222> LOCATION: (1)..(11)  
128 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
131 <400> SEQUENCE: 7  
133 Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro  
134 1 5 10  
137 <210> SEQ ID NO: 8  
138 <211> LENGTH: 11  
139 <212> TYPE: PRT  
C--> 140 <213> ORGANISM: Artificial/Unknown  
142 <220> FEATURE:  
143 <221> NAME/KEY: PEPTIDE

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144 <222> LOCATION: (1)..(11)  
145 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
148 <220> FEATURE:  
149 <221> NAME/KEY: MISC\_FEATURE  
150 <222> LOCATION: (11)..(11)  
151 <223> OTHER INFORMATION: X = alanine or another hydrophobic amino acid residue  
154 <400> SEQUENCE: 8  
OK-> 156 Gly Ser Ser Ser Gly Arg Gly Asp Ser Pro Xaa  
157 1 5 10  
160 <210> SEQ ID NO: 9  
161 <211> LENGTH: 5  
162 <212> TYPE: PRT  
C--> 163 <213> ORGANISM: Artificial/Unknown  
165 <220> FEATURE:  
166 <221> NAME/KEY: PEPTIDE  
167 <222> LOCATION: (1)..(5)  
168 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
171 <400> SEQUENCE: 9  
173 Arg Arg Lys Arg Arg  
174 1 5  
177 <210> SEQ ID NO: 10  
178 <211> LENGTH: 10  
179 <212> TYPE: PRT  
C--> 180 <213> ORGANISM: Artificial/Unknown  
182 <220> FEATURE:  
183 <221> NAME/KEY: PEPTIDE  
184 <222> LOCATION: (1)..(10)  
185 <223> OTHER INFORMATION: Synthesized with a peptide synthesizer  
188 <400> SEQUENCE: 10  
190 Pro Pro Arg Glu Val Val Pro Arg Pro Arg  
191 1 5 10

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 11